

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 101538,902
Source: PCT
Date Processed by STIC: 06-22-2005

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PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/538,902

DATE: 06/22/2005
TIME: 10:32:46

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06222005\J538902.raw

3 <110> APPLICANT: University of Medicine and Dentistry of New Jersey
4 Kaplan, Jeffrey B.
6 <120> TITLE OF INVENTION: Compositions and Methods for Enzymatic Detachment of
Bacterial and Fungal
7 Biofilms
9 <130> FILE REFERENCE: UMD-0015
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/538,902
C--> 11 <141> CURRENT FILING DATE: 2005-06-14
11 <150> PRIOR APPLICATION NUMBER: US 60/435,817
12 <151> PRIOR FILING DATE: 2002-12-20
14 <160> NUMBER OF SEQ ID NOS: 15
16 <170> SOFTWARE: PatentIn version 3.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1146
20 <212> TYPE: DNA
21 <213> ORGANISM: Actinobacillus actinomycetemcomitans strain CU1000N
23 <400> SEQUENCE: 1
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26 aattgttgcg taaaaggcaa ttccatataat ccgaaaaaaaaa caagtaccaa gcagaccgga 120
28 ttaatgtctgg acatcgccccg acatttttat tcaccgagg tgattaaatc ctttattgtat 180
30 accatcagcc ttccggcg taattttctg cacctgcatt ttccgacca taaaaactat 240
32 gcgatagaaa gccatttact taatcaacgt gcgaaaaatg ccgtgcaggg caaagacggt 300
34 atttatatta atccttatac cgaaaaagcca ttcttgagtt atcggcaact tgacgatatac 360
36 aaagcctatg ctaaggcaaa aggcattgag ttgattcccg aacttgacag cccgaatcac 420
38 atgacggcga tctttaaact ggtcaaaaaa gacagagggg tcaagtaccc tcaaggatta 480
40 aaatcacgccc aggtagatga tggaaattgat attactaatg ctgacagttt tactttatg 540
42 caatctttaa tgagttagt tattgatatt ttggcgaca cgagtccaga ttttcatatt 600
44 ggtggcgatg aatttggta ttctgtggaa agtaatcatg agtttattac gtagccaat 660
46 aaactatcct actttttaga gaaaaaaggg ttgaaaaccc gaatgtggaa tgacggatta 720
48 attaaaaata cttttgagca aatcaacccg aatattgaaa ttacttattt gagctatgtat 780
50 ggcgatacgc aggacaaaaa tgaagctgcc gagcggctg atatgcgggt cagttggcg 840
52 gagttgtctgg cgaaaaggctt tactgtccctg aactataatt cctattatct ttacattgtt 900
54 cccggaaagctt caccacccctt ctcgcaagat gcccgccttg cccggccaaaga tggatataaaa 960
56 aattgggatc ttgggttttggatggacga aacacaaaaa accgcgtaca aaataactcat 1020
58 gaaatagccg ggcgcagcatt atcgatctgg ggagaagatg caaaagcgt gaaagacgaa 1080
60 acaattcaga aaaacacgaa aagtttatttgaagcggtga ttcataagac gaatggggat 1140
62 gaggta
65 <210> SEQ ID NO: 2
66 <211> LENGTH: 381
67 <212> TYPE: PRT
68 <213> ORGANISM: Actinobacillus actinomycetemcomitans strain CU1000N
70 <400> SEQUENCE: 2
72 Met Asn Tyr Ile Lys Lys Ile Ile Leu Ser Leu Phe Leu Leu Gly Leu
73 1 5 10 15

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76 Phe Ser Val Leu Asn Cys Cys Val Lys Gly Asn Ser Ile Tyr Pro Gln
77 20 25 30
80 Lys Thr Ser Thr Lys Gln Thr Gly Leu Met Leu Asp Ile Ala Arg His
81 35 40 45
84 Phe Tyr Ser Pro Glu Val Ile Lys Ser Phe Ile Asp Thr Ile Ser Leu
85 50 55 60
88 Ser Gly Gly Asn Phe Leu His Leu His Phe Ser Asp His Glu Asn Tyr
89 65 70 75 80
92 Ala Ile Glu Ser His Leu Leu Asn Gln Arg Ala Glu Asn Ala Val Gln
93 85 90 95
96 Gly Lys Asp Gly Ile Tyr Ile Asn Pro Tyr Thr Gly Lys Pro Phe Leu
97 100 105 110
100 Ser Tyr Arg Gln Leu Asp Asp Ile Lys Ala Tyr Ala Lys Ala Lys Gly
101 115 120 125
104 Ile Glu Leu Ile Pro Glu Leu Asp Ser Pro Asn His Met Thr Ala Ile
105 130 135 140
108 Phe Lys Leu Val Gln Lys Asp Arg Gly Val Lys Tyr Leu Gln Gly Leu
109 145 150 155 160
112 Lys Ser Arg Gln Val Asp Asp Glu Ile Asp Ile Thr Asn Ala Asp Ser
113 165 170 175
116 Ile Thr Phe Met Gln Ser Leu Met Ser Glu Val Ile Asp Ile Phe Gly
117 180 185 190
120 Asp Thr Ser Gln His Phe His Ile Gly Gly Asp Glu Phe Gly Tyr Ser
121 195 200 205
124 Val Glu Ser Asn His Glu Phe Ile Thr Tyr Ala Asn Lys Leu Ser Tyr
125 210 215 220
128 Phe Leu Glu Lys Lys Gly Leu Lys Thr Arg Met Trp Asn Asp Gly Leu
129 225 230 235 240
132 Ile Lys Asn Thr Phe Glu Gln Ile Asn Pro Asn Ile Glu Ile Thr Tyr
133 245 250 255
136 Trp Ser Tyr Asp Gly Asp Thr Gln Asp Lys Asn Glu Ala Ala Glu Arg
137 260 265 270
140 Arg Asp Met Arg Val Ser Leu Pro Glu Leu Leu Ala Lys Gly Phe Thr
141 275 280 285
144 Val Leu Asn Tyr Asn Ser Tyr Tyr Leu Tyr Ile Val Pro Lys Ala Ser
145 290 295 300
148 Pro Thr Phe Ser Gln Asp Ala Ala Phe Ala Ala Lys Asp Val Ile Lys
149 305 310 315 320
152 Asn Trp Asp Leu Gly Val Trp Asp Gly Arg Asn Thr Lys Asn Arg Val
153 325 330 335
156 Gln Asn Thr His Glu Ile Ala Gly Ala Ala Leu Ser Ile Trp Gly Glu
157 340 345 350
160 Asp Ala Lys Ala Leu Lys Asp Glu Thr Ile Gln Lys Asn Thr Lys Ser
161 355 360 365
164 Leu Leu Glu Ala Val Ile His Lys Thr Asn Gly Asp Glu
165 370 375 380
168 <210> SEQ ID NO: 3
169 <211> LENGTH: 555
170 <212> TYPE: DNA

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Input Set : A:\PTO.RJ.txt
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171 <213> ORGANISM: *Actinobacillus ligniersii* strain 19393
 173 <400> SEQUENCE: 3
 174 gatcacgaga attatgcatt ggaaaagttct tatttggAAC aacgagaaga aaatgccgtt 60
 176 gagaaaaaacg gaaccttattt caatccgaaa acaaataagc cgtttctcac ttataaacag 120
 178 ctcaatgaaa ttatcttattt tgccaaagaa cgaatatttgg aaattgtgcc tgaagtcgat 180
 180 agcccgaatc atatgacggc gatTTTgtat ctTTTaaacc ttaaggacgg taaggagtt 240
 182 gtgaaaagggc tgaaatcgcc ttatcttgcg gaggaaatcg atattaataa ccctgaagcg 300
 184 gttgaaattt tcaaaacctt aatcggtgaa gtgatttata ttttggca ttccagccga 360
 186 cactttcata tcggccggaga cgaatttatg tatcggtcg aaaacaatca cgaatttatt 420
 188 cgTTtatgtaa atacgctaaa tgactttatt aataacaaag gactaattac ccgtatTTgg 480
 190 aacgacgggt tgattaaaaaa caatttaat gagcttaatc ggaatatcga aattacttat 540
 192 tggagctacg acgg 555
 195 <210> SEQ ID NO: 4
 196 <211> LENGTH: 185
 197 <212> TYPE: PRT
 198 <213> ORGANISM: *Actinobacillus ligniersii* strain 19393
 200 <400> SEQUENCE: 4
 202 Asp His Glu Asn Tyr Ala Leu Glu Ser Ser Tyr Leu Glu Gln Arg Glu
 203 1 5 10 15
 206 Glu Asn Ala Val Glu Lys Asn Gly Thr Tyr Phe Asn Pro Lys Thr Asn
 207 20 25 30
 210 Lys Pro Phe Leu Thr Tyr Lys Gln Leu Asn Glu Ile Ile Tyr Tyr Ala
 211 35 40 45
 214 Lys Glu Arg Asn Ile Glu Ile Val Pro Glu Val Asp Ser Pro Asn His
 215 50 55 60
 218 Met Thr Ala Ile Phe Asp Leu Leu Thr Leu Lys His Gly Lys Glu Tyr
 219 65 70 75 80
 222 Val Lys Gly Leu Lys Ser Pro Tyr Leu Ala Glu Glu Ile Asp Ile Asn
 223 85 90 95
 226 Asn Pro Glu Ala Val Glu Ile Ile Lys Thr Leu Ile Gly Glu Val Ile
 227 100 105 110
 230 Tyr Ile Phe Gly His Ser Ser Arg His Phe His Ile Gly Gly Asp Glu
 231 115 120 125
 234 Phe Ser Tyr Ala Val Glu Asn Asn His Glu Phe Ile Arg Tyr Val Asn
 235 130 135 140
 238 Thr Leu Asn Asp Phe Ile Asn Asn Lys Gly Leu Ile Thr Arg Ile Trp
 239 145 150 155 160
 242 Asn Asp Gly Leu Ile Lys Asn Asn Leu Asn Glu Leu Asn Arg Asn Ile
 243 165 170 175
 246 Glu Ile Thr Tyr Trp Ser Tyr Asp Gly
 247 180 185
 250 <210> SEQ ID NO: 5
 251 <211> LENGTH: 558
 252 <212> TYPE: DNA
 253 <213> ORGANISM: *Actinobacillus actinomycetemcomitans* strain IDH781
 255 <400> SEQUENCE: 5
 256 gatcatgaaa actatgcgtat agaaaggcat ttacttaatc aacgtgcggaa aaatgccgtt 60
 258 cagggcaaag acggtatttata tattatcct tataccggaa agccattttt gagttatcga 120
 260 caacttgacg atatcaaagc ctatgctaaag gcaaaaggca ttgagttgtat tcccgaaactt 180

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262	gatagtccga	atcacatgac	ggcgatctt	aaactggtgc	aaaaagacag	aggatcaag	240										
264	tatcttcaag	gattaaaatc	acgcccaggta	gatgatgaaa	ttgatattac	taatgctgac	300										
266	agatttgctt	ttatgcaatc	ttaatgagt	gaggttattg	atattttgg	cgacacgagt	360										
268	cagcatttc	atattggtgg	cgatgaattt	ggttattctg	tggaaaagtaa	tcatgagttt	420										
270	attacgtatg	ccaataaact	atcctacttt	ttagagaaaa	aggggttcaa	aaccgaaatg	480										
272	tggaatgacg	gattaattaa	aagtactttt	gagcaaatca	acccgaatat	tgaaattact	540										
274	tattggagct	atgatggc					558										
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278	<211>	LENGTH:	186														
279	<212>	TYPE:	PRT														
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285	1						5				10				15		
288	Glu	Asn	Ala	Val	Gln	Gly	Lys	Asp	Gly	Ile	Tyr	Ile	Asn	Pro	Tyr	Thr	
289							20				25				30		
292	Gly	Lys	Pro	Phe	Leu	Ser	Tyr	Arg	Gln	Leu	Asp	Asp	Ile	Lys	Ala	Tyr	
293							35				40				45		
296	Ala	Lys	Ala	Lys	Gly	Ile	Glu	Leu	Ile	Pro	Glu	Leu	Asp	Ser	Pro	Asn	
297							50				55				60		
300	His	Met	Thr	Ala	Ile	Phe	Lys	Leu	Val	Gln	Lys	Asp	Arg	Gly	Ile	Lys	
301	65						65				70				75		80
304	Tyr	Leu	Gln	Gly	Leu	Lys	Ser	Arg	Gln	Val	Asp	Asp	Glu	Ile	Asp	Ile	
305							85				90				95		
308	Thr	Asn	Ala	Asp	Ser	Ile	Ala	Phe	Met	Gln	Ser	Leu	Met	Ser	Glu	Val	
309							100				105				110		
312	Ile	Asp	Ile	Phe	Gly	Asp	Thr	Ser	Gln	His	Phe	His	Ile	Gly	Gly	Asp	
313							115				120				125		
316	Glu	Phe	Gly	Tyr	Ser	Val	Glu	Ser	Asn	His	Glu	Phe	Ile	Thr	Tyr	Ala	
317							130				135				140		
320	Asn	Lys	Leu	Ser	Tyr	Phe	Leu	Glu	Lys	Gly	Leu	Lys	Thr	Arg	Met		
321	145						145				150				155		160
324	Trp	Asn	Asp	Gly	Leu	Ile	Lys	Ser	Thr	Phe	Glu	Gln	Ile	Asn	Pro	Asn	
325							165				170				175		
328	Ile	Glu	Ile	Thr	Tyr	Trp	Ser	Tyr	Asp	Gly							
329							180				185						
332	<210>	SEQ ID NO:	7														
333	<211>	LENGTH:	558														
334	<212>	TYPE:	DNA														
335	<213>	ORGANISM:	Haemophilus aphrophilus	strain	NJ8700												
337	<400>	SEQUENCE:	7														
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340	ttaaataaaaa	acggaattta	tattaatcct	tacaccaata	agcctttctt	gagttatcaa									120		
342	cagttggatg	acattaaagc	atatgcaaaa	ttaaaaggta	ttgagcttat	tcccgaaatta									180		
344	gatagccccga	atcacatgac	agcgattttt	accttattaa	aaaaagaaaa	aggaaaaaat									240		
346	tatcttcaat	cgttaaaaatc	accacaaaat	gatgaggaaa	ttagcatac	caatccggac									300		
348	agcatttgcatt	ttatgcaatc	cttattaaca	gagtaattc	atacccttgg	cgatagcacc									360		
350	aagcatttttc	atattggcgg	agatgagttt	ggttatgatg	aaaatagtaa	tcatgaattt									420		
352	attacctatg	ccaataaattt	ggctgatttt	ttaagagaaa	aaggattaaa	aactcgaattt									480		

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354 tggaatgatg gtttaattaa aaataccata gatcaattaa atcctaataat tgaaattacc 540
 356 tactggagtt acgacggc 558
 359 <210> SEQ ID NO: 8
 360 <211> LENGTH: 186
 361 <212> TYPE: PRT
 362 <213> ORGANISM: Haemophilus aphrophilus strain NJ8700
 364 <400> SEQUENCE: 8
 366 Asp His Glu Asn Tyr Ala Leu Glu Ser Arg Leu Leu Asn Gln Arg Ala
 367 1 5 10 15
 370 Glu Asn Ala Ile Leu Asn Lys Asn Gly Ile Tyr Ile Asn Pro Tyr Thr
 371 20 25 30
 374 Asn Lys Pro Phe Leu Ser Tyr Gln Gln Leu Asp Asp Ile Lys Ala Tyr
 375 35 40 45
 378 Ala Lys Leu Lys Gly Ile Glu Leu Ile Pro Glu Leu Asp Ser Pro Asn
 379 50 55 60
 382 His Met Thr Ala Ile Phe Thr Leu Leu Lys Lys Glu Lys Gly Lys Asn
 383 65 70 75 80
 386 Tyr Leu Gln Ser Leu Lys Ser Pro Gln Asn Asp Glu Glu Ile Ser Ile
 387 85 90 95
 390 Thr Asn Pro Asp Ser Ile Ala Phe Met Gln Ser Leu Leu Thr Glu Val
 391 100 105 110
 394 Ile His Thr Phe Gly Asp Ser Thr Lys His Phe His Ile Gly Gly Asp
 395 115 120 125
 398 Glu Phe Gly Tyr Asp Glu Asn Ser Asn His Glu Phe Ile Thr Tyr Ala
 399 130 135 140
 402 Asn Lys Leu Ala Asp Phe Leu Arg Glu Lys Gly Leu Lys Thr Arg Ile
 403 145 150 155 160
 406 Trp Asn Asp Gly Leu Ile Lys Asn Thr Ile Asp Gln Leu Asn Pro Asn
 407 165 170 175
 410 Ile Glu Ile Thr Tyr Trp Ser Tyr Asp Gly
 411 180 185
 414 <210> SEQ ID NO: 9
 415 <211> LENGTH: 555
 416 <212> TYPE: DNA
 417 <213> ORGANISM: Actinobacillus pleuropneumoniae strain IA5
 419 <400> SEQUENCE: 9
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 422 gagaaaaaacg gaaccttattt caatccgaaa acaaataagc cgtttctcac ttataaacag 120
 424 ctcaatgaaa ttatctatta tgccaaagaa cgaatattg aaattgtgcc tgaagtcgat 180
 426 agcccgaaatc atatgacggc gatTTTgtat ctttaaccc ttaagcacgg aaaggaatac 240
 428 gtaaaagggc taaaatcgcc ttatatcgcc gagggaaatcg atattaataa ccccgaaagcg 300
 430 gttgaagttt taaaaacctt aatcggtgaa gtgatctata ttttcggaca ttcaagccgg 360
 432 catttccata tcggcggaga tgaatttagc tatcggtcg aaaataatca tgaatttatt 420
 434 cgttatgtga ataccttaaa tgatTTTatc aattccaaag ggctaattac ccgtgtttgg 480
 436 aatgacgggt tgatcaaaaa caacttaagc gaactcaata aaaacattga aatcacttac 540
 438 tggagctacg acggc 555
 441 <210> SEQ ID NO: 10
 442 <211> LENGTH: 185
 443 <212> TYPE: PRT

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/22/2005
PATENT APPLICATION: US/10/538,902 TIME: 10:32:48

Input Set : A:\PTO.RJ.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 1

Seq#:13; N Pos. 3

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 6

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:509 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0

L:540 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0